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ON August 16, 2001

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:

August 16, 2001 Bruck, et al.

Serial No.: 09/509,239 Group Art Unit No.: 1648

Filed: March 23, 2000

Examiner: U. Winkler

For:

"Fusion Proteins Comprising HIV-1 Tat and/or Nef Proteins"

Assistant Commissioner for Patents

Attn: Chief Draftsman

Washington, D.C. 20231

#### TRANSMITTAL OF FORMAL DRAWINGS

In response to the Notice of Informal Drawings mailed on July 17, 2000 attached please find:

the formal drawings for this application with each sheet indicating the Serial (a) Number of Sheets: 18 Number and the Group Art Unit.

(b) a copy of the Notice of Informal Drawings.

Respectfully submitted,

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FIG. 1A Map of plasmid pRIT14586

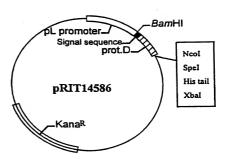


FIG. 1B Coding sequence of the first 127 amino acids of protein D and multiple cloning site. The signal sequence is underlined.

### Bam#| As Pro Lys | Thr Leu | Ala | Leu | Ser | Leu | Ala | Ala | Cly | Val | Leu | Ala | Cly | Cgr | Ggr | Ggr

The amino acid sequence of Figure 1 relates to Seq. ID no. 7 and the he nucleic acid of sequence of Figure 1 relates to Seq. ID no. 6.

# FIG. 2A

The DNA and amino acid sequences of Nef-His; Tat-His; Nef-Tat-His fusion and mutated Tat is illustrated.

#### Pichia-expressed constructs (plain constructs)

⇒ Nef - HIS

DNA sequence (Seq. ID. No. 8)

ATGGGTGGCAAGTGGTCAAAAGTAGTGTGGTTGGTTGGCCTACTGTAAGGGAAAGA
ATGAGACGAGCTGACACAGATTGGGTTGGAGACATCTCGAGACCTGGAA
ATGAGACGAGCTGACCAGATTGGGATGCGTTGCACACTTGTGAGACCTGGAA
AAACATGGAGCAACACAAGTAGCAGTACCACTTGTGCTTGTGCTTG
CTAGAAGCACAAGAGGAGGAGGAGGTGGTTTTCCAGTCACCTCAGGTACCTTTA
AGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAAGGG
GGACTGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATC
ACACACAAGGCTACTTCCCTGATTGGCAGAACTACACCAGGGCCAGGGGTC
AGATATCCACTCACCTTTTGGATGGTGCTACAAGCTTAGTACCAGTTGAGCCAGATAAG
GTAGAAGAGGCCAATAAAGGAGAAGACCAGCTTGTTACACCCTGTGAGCCTGCAT
TCATCACGTGGCCCGAGAGAAGTGTTTAGAGTGGAGGTTTGACACCCCTAGCA
TTTCATCACGTGGCCCGAGAGCTTGCATCCGGAGTACTTCAAGACTAGTGGC
CACCATCACCATTAA

#### Protein sequence (Seq. ID. No. 9)

MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAW LEAQEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWI YHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLH GMDDPEREVLEWRFDSRLAFHHVARELHPEYFRNCTSGHHHHHH.

⇒ Tat - HIS

DNA sequence (Seq. ID. No. 10)

ATGGAGCCAGTAGATCCTAGACTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAA
ACTGCTTGTACCAATTGCTATTGTAAAAAGTGTTTGCTTTCATTGCCAAGTTTTGTTTA
ATAACAAAAGCCTTAGGCATCTCCTATGGCAAGAAGAAGCGGACAAGCAGCAACGAGCAAGA
CCTCCTCAAGGCAGTCAGACTCATCAAGTTTCTCTTATCAAAGCAACCCACCTCCCAA

# FIG. 2B

TCCCGAGGGGACCCGACAGGCCCGAAGGAAACTAGTGGCCACCATCACCATCACCAT
TAA

#### Protein sequence (Seq. ID. No. 11)

MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRR PPOGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH.

#### ⇒ Nef - Tat - HIS

#### DNA sequence (Seq. ID. No. 12)

ATGGGTGGCAAGTGGTCAAAAAGTAGTGTGGTTGGATGGCCTACTGTAAGGGAAAGA ATGAGACGAGCTGAGCCAGCAGCAGCAGCAGCAGCACCATCTCGAGACCTGGAA AAACATGGAGCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGCTTGTGCCTGG CTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTA AGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGGG GGACTGGAAGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATC TACCACACACAGGCTACTTCCCTGATTGGCAGAACTACACCAGGGCCAGGGGTC AGATATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAG GTAGAAGAGGCCAATAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCAT GGAATGGATGACCCTGAGAGAGAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCA TTTCATCACGTGGCCCGAGAGCTGCATCCGGAGTACTTCAAGAACTGCACTAGTGAG CCAGTAGATCCTAGACTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAAACTGCT AAAGCCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGCGAGACCTCCT CAAGGCAGTCAGACTCATCAAGTTTCTCTATCAAAGCAACCCACCTCCCAATCCCGA GGGGACCCGACAGGCCCGAAGGAAACTAGTGGCCACCATCACCATCACCATTAA

#### Protein sequence(Seq. ID. No. 13)

MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAW LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWI YHTQGYFPDWQNYTFGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLH GMDDFEREVLEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTA CTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRPPQGSQTHQVSLSKQPTSQSR GDDTGBKETSGHHHHHH

#### E.coli-expressed c nstructs (fusion constructs)

⇒ LipoD-Nef-HIS

## FIG. 2C

#### DNA sequence (Seq. ID. No. 14)

Nucleotides corresponding to the Prot D Fusion Partner are in bold.

The Lipidation Signal Sequence is underlined. After processing, the cysteine coded by the TGT codon, indicated with a star, becomes the amino terminal residue which is then modified by covalently bound fatty acids.

ATGGATCCAAAAACTTTAGCCCTTTCTTTATTAGCAGCTGGCGTACTAGCAGGTTGT AGCAGCCATTCATCAAATATGGCGAATACCCAAATGAAATCAGACAAAATCATTATT GCTCACCGTGGTGCTAGCGGTTATTTACCAGAGCATACGTTAGAATCTAAAGCACTT GCTTTTGCACAACAGGCTGATTATTTAGAGCAAGATTTAGCAATGACTAAGGATGGT CGTTTAGTGGTTATTCACGATCACTTTTTAGATGGCTTGACTGATGTTGCGAAAAAA TTCCCACATCGTCATCGTAAAGATGGCCGTTACTATGTCATCGACTTTACCTTAAAA GAAATTCAAAGTTTAGAAATGACAGAAAACTTTGAAACCATGGGTGGCAAGTGGTCA AAAAGTAGTGTGGTTGGATGGCCTACTGTAAGGGAAAGAATGAGACGAGCTGAGCCA GCAGCAGATGGGGTGGGAGCAGCATCTCGAGACCTGGAAAAAACATGAGCAATCACA AGTAGCAATACAGCAGCTACCAATGCTGCTTGTGCCTGGCTAGAAGCACAAGAGGAG GAGGAGGTGGGTTTTCCAGTCACCTCAGGTACCTTTAAGACCAATGACTTACAAG GCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGGGGGGACTGGAAGGGCTAATT TTCCCTGATTGGCAGAACTACACCAGGGCCAGGGGTCAGATATCCACTGACCTTT GGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAGGTAGAAGAGGCCAATAAA GGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCTGAG AGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACGTGGCCCGA GAGCTGCATCCGGAGTACTTCAAGAACTGCACTAGTGGCCACCATCACCATCACCAT TAA

Protein sequence of the processed lipidated ProtD-Nef-HIS protein (Seq. ID. No. 15)

(Amino-acids corresponding to Prot D fusion partner are in bold)

CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKD GRLVVIHDBFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKW SKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQE EEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRQDILDLWIYHTQG YFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP EREVLEWRFDSRLAFHHVARELHPEYFKNCTSGHHHHHH

⇒ LipoD-Nef-Tat-HIS

DNA sequence (Seq. ID. No. 16)

# FIG. 2D

Nucleotides corresponding to the Prot D Fusion Partner are in bold.

The Lipidation Signal Sequence is underlined. After processing, the cysteine coded by the TGT codon, indicated with a star, becomes the amino terminal residue which is then modified by covalently bound fatty acids.

ATGGATCCAAAAACTTTAGCCCTTTCTTTATTAGCAGCTGGCGTACTAGCAGGTTGT AGCAGCCATTCATCAAATATGGCGAATACCCAAATGAAATCAGACAAAATCATTATT GCTCACCGTGGTGCTAGCGGTTATTTACCAGAGCATACGTTAGAATCTAAAGCACTT GCGTTTGCACAACAGGCTGATTATTTAGAGCAAGATTTAGCAATGACTAAGGATGGT CGTTTAGTGGTTATTCACGATCACTTTTTAGATGGCTTGACTGATGTTGCGAAAAAA TTCCCACATCGTCATCGTAAAGATGGCCGTTACTATGTCATCGACTTTACCTTAAAA GAAATTCAAAGTTTAGAAATGACAGAAAACTTTGAAACCATGGGTGGCAAGTGGTCA AAAAGTAGTGTGGTTGGATGGCCTACTGTAAGGGAAAGAATGAGACGAGCTGAGCCA GCAGCAGATGGGGTGGGAGCAGCATCTCGAGACCTGGAAAACATGGAGCAATCACA AGTAGCAATACAGCAGCTACCAATGCTGCTTGTGCCTGGCTAGAAGCACAAGAGGAG GAGGAGGTGGGTTTTCCAGTCACCTCAGGTACCTTTAAGACCAATGACTTACAAG GCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAGGGGGGGACTGGAAGGGCTAATT TTCCCTGATTGGCAGAACTACACACCAGGGCCAGGGGTCAGATATCCACTGACCTTT GGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAGGTAGAAGAGGCCAATAAA GGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCTGAG AGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACGTGGCCCGA GAGCTGCATCCGGAGTACTTCAAGAACTGCACTAGTGAGCCAGTAGATCCTAGACTA GAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAAACTGCTTGTACCAATTGCTATTGT AAAAAGTGTTGCTTTCATTGCCAAGTTTGTTTCATAACAAAAGCCTTAGGCATCTCC TATGGCAGGAAGAGCGGAGACAGCGAAGACCTCCTCAAGGCAGTCAGACTCAT CAAGTTTCTCTATCAAAGCAACCCACCTCCCAATCCCGAGGGGACCCGACAGGCCCG AAGGAAACTAGTGGCCACCATCACCATCACCATTAA

Protein sequence of the processed lipidated ProtD-NEF-TAT-HIS protein (Seq. ID. No. 17)

(Amino-acids corresponding to Prot D fusion partner are in bold)

CSSESSMMANTOMESDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKD
GRLVVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKW
SKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQE
EEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQG
YFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP
EREVLEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHFGSQPKTACTNCY
CKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTG
PKETSGHHHHHH.

#### ⇒ ProtD-Nef -HIS

#### DNA sequence (Seq. ID. No. 18)

Nucleotides corresponding to the Prot D Fusion Partner are in bold.

ATGGATCCAAGCAGCCATTCATCAAATATGGCGAATACCCAAATGAAATCAGACAAA ATCATTATTGCTCACCGTGGTGCTAGCGGTTATTTACCAGAGCATACGTTAGAATCT AAAGCACTTGCGTTTGCACAACAGGCTGATTATTTAGAGCAAGATTTAGCAATGACT AAGGATGGTCGTTTAGTGGTTATTCACGATCACTTTTTAGATGGCTTGACTGATGTT GCGAAAAATTCCCACATCGTCATCGTAAAGATGGCCGTTACTATGTCATCGACTTT ACCTTAAAAGAAATTCAAAGTTTAGAAATGACAGAAAACTTTGAAACCATGGGTGGC AAGTGGTCAAAAAGTAGTGTGGTTGGATGGCCTACTGTAAGGGAAAGAATGAGACGA GCTGAGCCAGCAGCAGATGGGGTGGGAGCAGCATCTCGAGACCTGGAAAAACATGGA GCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGCTTGTGCCTGGCTAGAAGCA CAAGAGGAGGAGGAGGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAATG ACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAA GGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCACACA CAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCAGGGGTCAGATATCCA CTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAGGTAGAAGAG GCCAATAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGAT GACCCTGAGAGAGAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCAC GTGGCCCGAGAGCTGCATCCGGAGTACTTCAAGAACTGCACTAGTGGCCACCATCAC CATCACCATTAA

#### Protein sequence (Seq. ID. No. 19)

(Amino-acids corresponding to Prot D fusion partner are in bold)

MDPSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYL EQDLAMTKDGRLVVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLK EIQSLEMTENFETMGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDL EKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSH FLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGW CYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFH HVARELHPEYFKNCTSGHHHHHHH.

#### ⇒ ProtD-Nef -Tat-HIS

DNA sequence (Seq. ID. No. 20)

# FIG. 2F

Nucleotides corresponding to the Prot D Fusion Partner are in bold.

ATGGATCCAAGCAGCCATTCATCAAATATGGCGAATACCCAAATGAAATCAGACAAA ATCATTATTGCTCACCGTGGTGCTAGCGGTTATTTACCAGAGCATACGTTAGAATCT AAAGCACTTGCGTTTGCACAACAGGCTGATTATTTAGAGCAAGATTTAGCAATGACT AAGGATGGTCGTTTAGTGGTTATTCACGATCACTTTTTAGATGGCTTGACTGATGTT GCGAAAAAATTCCCACATCGTCATCGTAAAGATGGCCGTTACTATGTCATCGACTTT ACCTTAAAAGAAATTCAAAGTTTAGAAATGACAGAAAACTTTGAAACCATGGGTGGC AAGTGGTCAAAAAGTAGTGTGGTTGGATGGCCTACTGTAAGGGAAAGAATGAGACGA GCTGAGCCAGCAGCAGGTGGGGAGCAGCATCTCGAGACCTGGAAAAACATGGA GCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGCTTGTGCCTGGCTAGAAGCA CAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACCCTCAGGTACCTTTAAGACCAATG ACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGGGGGGACTGGAA GGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCACACA CAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCCAGGGGTCAGATATCCA CTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGATAAGGTAGAAGAG GCCAATAAAGGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGAT GACCCTGAGAGAGAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCAC GTGGCCCGAGAGCTGCATCCGGAGTACTTCAAGAACTGCACTAGTGAGCCAGTAGAT CCTAGACTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAAACTGCTTGTACCAAT GGCATCTCCTATGGCAGGAAGAGCGGAGACAGCGACGAAGACCTCCTCAAGGCAGT CAGACTCATCAAGTTTCTCTATCAAAGCAACCCACCTCCCAATCCCGAGGGGACCCG ACAGGCCCGAAGGAAACTAGTGGCCACCATCACCATCACCATTAA

## Protein sequence (Seq. ID. No. 21)

(Amino-acids corresponding to Prot D fusion partner are in bold)

MDPSSHSSMMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMT KDGRLVVIHDHFLDGLTDVAKKFPHRHHRDGRYYVIDFTLKEIQSLEMTENFETMGG KWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLHIYHT QGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMD DPEREVLEWFFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTN CYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDP TGPKETSGHHHHHHH.

#### ⇒ Tat-MUTANT-HIS

# FIG. 2G

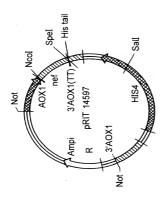
ATGGAGCCAGTAGATCCTAGACTAGAGCCCTGGAAGCATC	40
CAGGAAGTCAGCCTAAAACTGCTTGTACCAATTGCTATTG	80
TAAAAAGTGTTGCTTTCATTGCCAAGTTTGTTTCATAACA	120
GCTGCCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGAC	160
AGCGACGAAGACCTCCTCAAGGCAGTCAGACTCATCAAGT	200
TTCTCTATCAAAGCAACCCACCTCCCAATCCAAAGGGGAG	240
CCGACAGGCCCGAAGGAAACTAGTGGCCACCATCACCATC	280
ACCATTAA	288
Puntain annual/Cap ID No. 221	
Protein sequence(Seq. ID. No. 23)	
Mutated amino-acids in Tat sequences are in bold.	
MEPVDPRLEPWKHPGSOPKTACTNCYCKKCCFHCOVCFIT	40
AALGISYGRKKRORRRPPOGSOTHOVSLSKOPTSOSKGE	80
PTGPKETSGHHHHHH.	95
rioritationininini.	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
⇒Nef-Tat-Mutant-HIS	
DNA sequence(Seq. ID. No. 24)	
${\tt ATGGGTGGCAAGTGGTCAAAAAGTAGTGTGGTTGGATGGC}$	40
CTACTGTAAGGGAAAGAATGAGACGAGCTGAGCCAGCAGC	80
AGATGGGGTGGGAGCCAGCATCTCGAGACCTGGAAAAACAT	120
GGAGCAATCACAAGTAGCAATACAGCAGCTACCAATGCTG	160
CTTGTGCCTGGCTAGAAGCACAAGAGGAGGAGGAGGTGGG	200
TTTTCCAGTCACACCTCAGGTACCTTTAAGACCAATGACT	240
TACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAA	280
AGGGGGGACTGGAAGGGCTAATTCACTCCCAACGAAGACA	320
AGATATCCTTGATCTGTGGATCTACCACACACACAGGCTAC	360
TTCCCTGATTGGCAGAACTACACACCAGGGCCAGGGGTCA	400
GATATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACC	440
AGTTGAGCCAGATAAGGTAGAAGAGGCCAATAAAGGAGAG	480
AACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGG	520
ATGACCCTGAGAGAGAGTGTTAGAGTGGAGGTTTGACAG	560
CCGCCTAGCATTTCATCACGTGGCCCGAGAGCTGCATCCG	600
GAGTACTTCAAGAACTGCACTAGTGAGCCAGTAGATCCTA	640
GACTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAAAC	680
TGCTTGTACCAATTGCTATTGTAAAAAGTGTTGCTTTCAT	720
TGCCAAGTTTGTTTCATAACAGCTGCCTTAGGCATCTCCT	760
ATGGCAGGAAGAGCGGAGACAGCGACGAAGACCTCCTCA	800
AGGCAGTCAGACTCATCAAGTTTCTCTATCAAAGCAACCC	
ACCTCCCAATCCAAAGGGGAGCCGACAGGCCCGAAGGAAA	880
CTAGTGGCCACCATCACCATTAA	909

# FIG. 2H

# <u>Protein sequence (Seq. ID. No. 25)</u> Mutated amino-acids in Tat sequence are in bold.

Commission of the contract of	
GAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMT	80
YKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY	120
FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGE	160
NTSLLHPVSLHGMDDPEREVLEWRFDSRLAFHHVARELHP	200
EYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH	240
CQVCFIT <b>AA</b> LGISYGRKKRRQRRRPPQGSQTHQVSLSKQP	280
TSOSKGEPTGPKETSGHHHHHH .	302

FIG. 3 Map of pRIT14597 integrative vector



MCS POLYLINKER: nef gene inserted between Ncol and Spel sites.

Eco RI	TTCGAA.ACC.ATGGCCGCGGACTAGT.GGC.CAC.CAT.CAC.CAT.CAC.CAT.TAA.CGGAATTC	Thr Ser Glv. His His His His His
Spe $I$	CCGCGGACTAGT.GGC.	Thr Ser Glv
Nco I	ACC.ATGG	
Acu II	TTCGAA.	

The amino acid sequence of Figure 3 relates to Seq. ID no. 27 and the nucleic acid sequence of Figure 3 relates to Seq. ID. No. 26.



9 9



5: MW (175/83/62,5/47,5/32,5/25/16,5/6,5 kDa 6: TNH/23 SP eluate (400 ng) 7: TNH/23 Purified bulk (400 ng) 8: TNH/22 Purified bulk (400 ng)

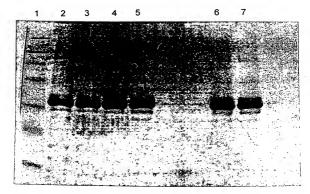
Daiichi Silver Staining





Blot Tat2

FIG. 5 SDS-PAGE: Nef-Tat-his fusion protein



### Coomassie blue G250

- 1: MW (175/83/62,5/47,5/32,5/25/16,5/6,5 kDa)
- 2: TNH/23 SP eluate (4 µg)
- 3: TNH/23 Superdex200 elµate (4 µg)
- 4: TNH/23 Purified bulk (4 µg)
- 5: TNH/22 Purified bulk (4 µg)
- 6: TNH/23 Purified bulk (4 µg) / non reducing conditions
- 7: TNH/22 Purified bulk (4 µg) / non reducing conditions

FIG. 6A Tat-specific antibody titers and isotypes

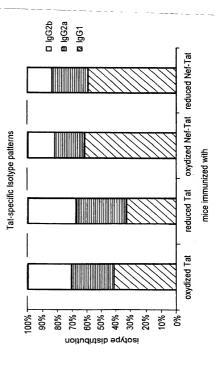


FIG. 6B Tat-specific antibody titers and isotypes

		midpoint titers	titers			
group	immunization	βj	lgG1	lgG2a	lgG2b	ratio lgG1/lgG2a
-	reduced Tat	212799	123242	62697	55763	1,966
5	reduced Nef-Tat	75676	84046	18449	11692	4,556
က	adjuvant only	<4000	<4000	<4000	<4000	

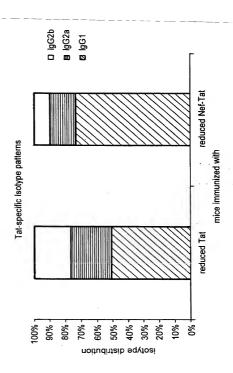


FIG. 7 Antigen-specific lymphoproliferative response of pooled lymph node cells

Data expressed as stimulation index	Group 3 adjuvant only		-0-	-	© 5µg/ml © 1µg/ml © 0.2µg/ml	adjuvant only
ssed as stim	Group 2 reduced Nef-Tat	115 201 145	197 174 142	-		reduced Nef-Tat mice immunized with
Data expres	Group 1 reduced Tat	140 125 92	146 113 84	-		reduced mice imm
		reduced Tat 5µg/ml 1µg/ml 0.2µg/ml	reduced Nef-Tat 5µg/ml 1µg/ml 0.2µg/ml	mednim	index of etimulation	reduced Tat
				_	noitalumits to xebni	
(3H) Thymidine incorporation in cpm	Group 3 adjuvant only	789 415 397	483 245 383	571	© 5µg/ml ⊡ 1µg/ml □ 0.2µg/ml	adjuvant only
ine incorpon	Group 2 reduced Nef-Tat	18511 32346 23408	31694 28094 22891	161		reduced Nef-Tat mice immunized with
			1			
(3H) Thymid	Group 1 reduced Tat	41967 37609 27640	43882 33865 25079	300		reduced mice imm
(3H) Thymid	Group 1 reduced Tat	reduced Tat 41967 5µg/ml 37609 1µg/ml 27640	reduced Nef-Tat 43882 5/49/ml 33865 1/49/ml 25079	meduim 300	index of atimulation 80 00 00 00 00 00 00 00 00 00 00 00 00	reduced Tat



